

Figure 1A

S. pneumoniae -----MKTRITELLKIDYPIFQGGMAWADGDLAGAVSKAGGLCIIIGGGNAP. KEVVKANIDKIKSLTDKPFGVN
Ent. faecalis MKCTYLRTKGRIKSMNQELCELLGINYPFQGGMAWADASLASAVSNAGGLCHIAGGNAP. KEVVKKEIKKVKELTQPFGVN
C. difficile -----MNKICKILNIKYPVIOGGMAWATASLASAVSNAGGLCIIAAGNAP. KEAIJKGETVECKKLTKPFGVN
P. aeruginosa -----MGVFRTRFTETFGVEHPIMQGGMOWVGRAEAAAANAGGLATLSALTQSSPEALAAEIARCRELTDRPFGVN

 IMLL...SPFV. EDIVDVLVIEEGVIVVITGAGNESKYMEREHEAGIIVIPVVPSSVALAKRMEEKIGADAVIAEGMSAGGHIG...KLTTMTLIVRQVATAS
 IMLL...SPFA. DEIVDVLVCEEQPVVITGAGNEAKYMARFKEHNKIVIPVVPSSVALAKRMEEKIGADAVIFEGMSAGGHIG...KLTTMSGPQIVDAWS
 VMLM...SPFV. DDIIIDLIIIEEKVIVVITGAGNEAKYMDRIKEAGTKVIPVVPSSVALAKRMEEKIGADAVIAEGMSAGGHIG...ELTTMVLVLPQVADAVN
 LTLPPTQKPVPYASYRAAIIIBAGIRVVIETAGNDEGEHIAEFRRHGVKVIHKCTAVRHALKAERLGYDAVSIDGPFECAGHPCEDDITPGIVLLPAAANRER

 PAD
 IPVIAAGGIADGEGAAAGFMLGAPAVQVGTRFVVAKESENAPNYKEKVLKARDIDTTISAQHFGBAVRAIKNQITRDFELAEKDAFKQEDPDLEIFEQM
 IPVIAAGGIIGDGRGMAAAEMLCAEAVOLGTRFLIAKECNVHEDYKOKVLKARDIDAVITCQHFGBVRTIKNKLTAQYNQLEKQELQEVVPDLEMPEKI
 IPVIAAGGIIVDGRGIAASFALGASAVQVGTRFICSEECVHSNYNLVLAQKDRDAIVTGRSTGHPVRTIKNKLKEFLKMEQNGATPEE...LDKK
 VPIIASGGFADGRGLVAALALGADAINMGTRFLATRSCPIHPAVKAAIARAADERSTDILIMRSLRNTARVARNAISQEVLAIE...ARGGAGYADIAALV

 GAGALAKAVVHGDVPGGSVMAGQIAGLVSKETAAEILKDIYYGAAKKIQEEASRWTGVRND
 GQGALRKAVVVDGDMYGSVMAGQIAGLIKKEETACEITIDSLMSECKAIVHKMNQRWG-----
 GTGALRFATVDGDIENGSFMAGQSAAMVKEITPCKEIIIEAMVNQAREIMPAIEL-----
 SGQRGRQVYQQGDTDLCIWSAGMVQGLIDDEPACELLRDIVVEQARQLVQRLEGMLAGV---

Figure 1B

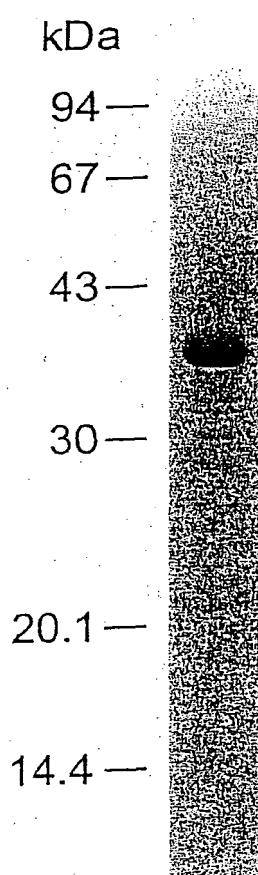


Figure 2A

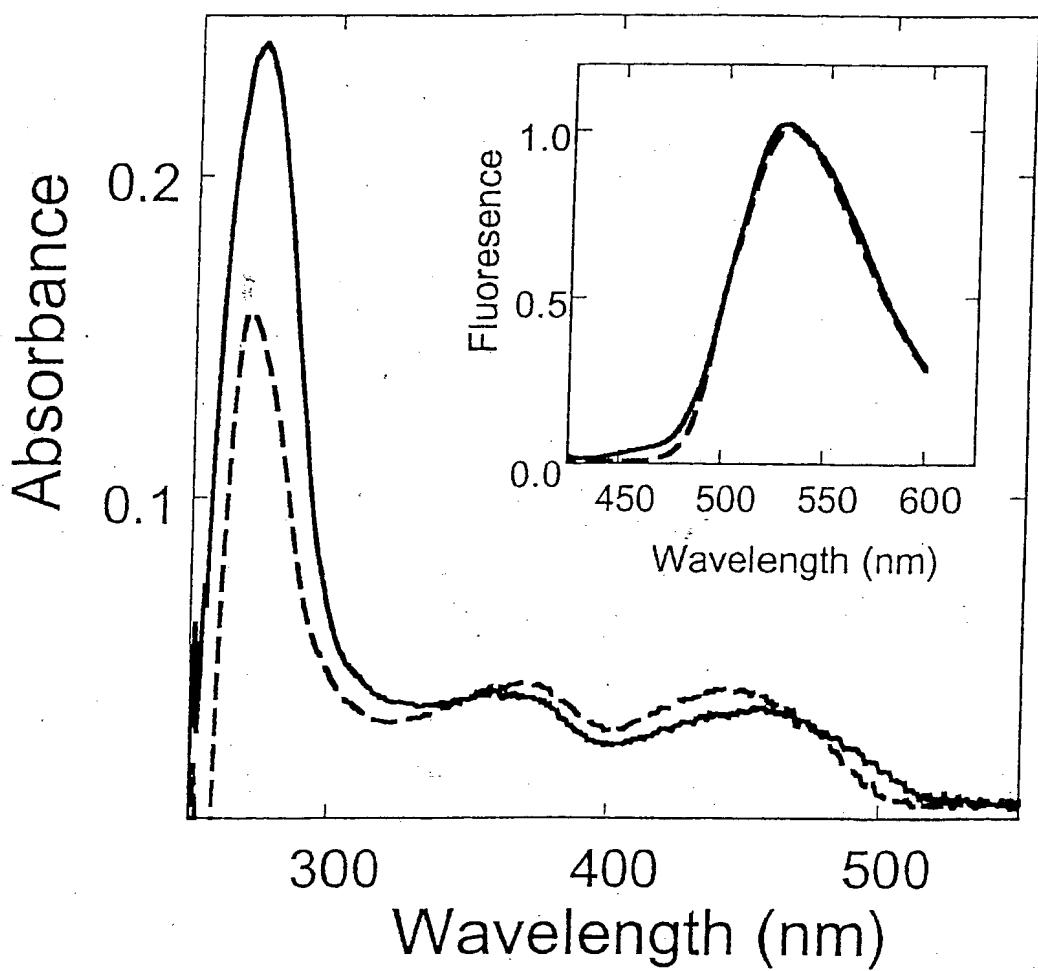


Figure 2B

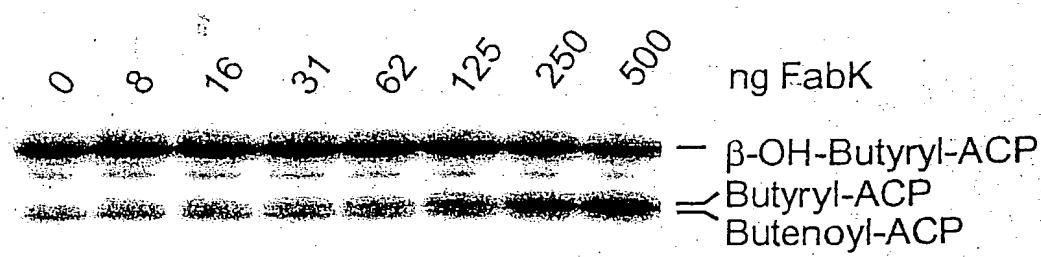


Figure 2C

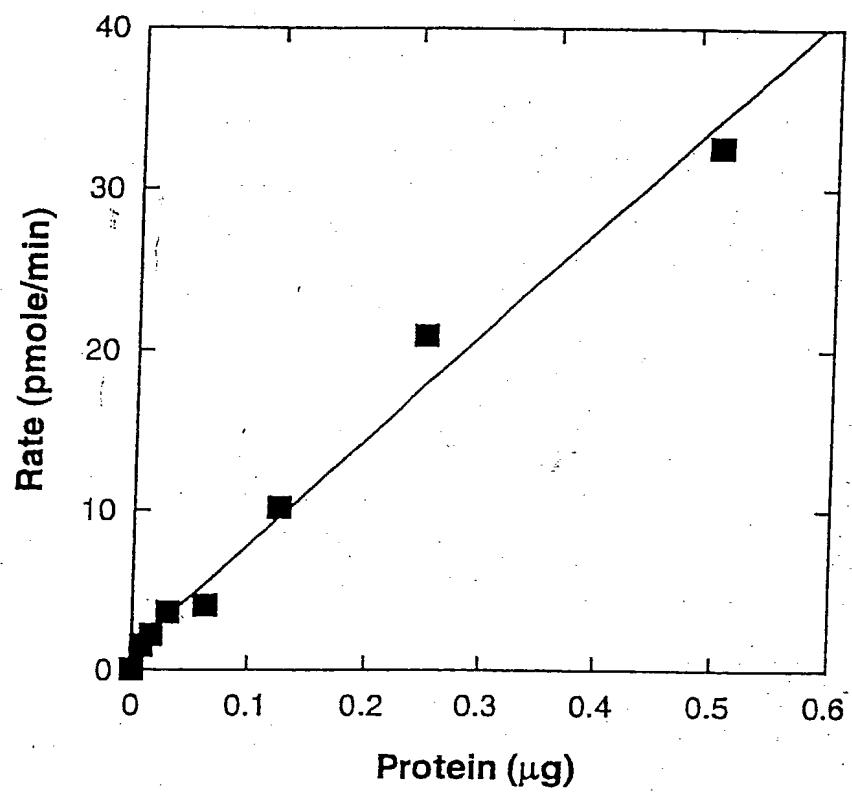


Figure 2D

FABL_BACSU -----MEQNRCALVTCSSRGVCKAAIRL..ENGYNIVINVARSKKAALETABEIE..KLGVKVLVVKAAVGQPAAKEMFOCIDET
FABL_HPYLO MNGSNHMKNKTLVUSGATRGIGKAFURFA..QSGVNIAFTXNKVEEANKTIEDVEQKYSIKAKAYSLAVLEPEQYTELFKOIDAD
FABI_ECOLI ---MGFLSGCRILVTGVASKLSIAYGTAQAMHREGAAIAFTVQNDKLKGR..VEEFAAQIGSDI..VLQCDVAEDASIDTMAELGKV

EGRILQVEVNN..A.....ASGVLRPVMELEETHWDWTMNINAKALI.FCAQEAAKLMKEKNGGGHIVSISSLGSIKYENYTTVGUSKAALEALTRYLAVE
FDRVDFPTSN..AIIYGRSVVCGFAPPFMRLKPKGlnNIYTATVLA5VGAQEAAKRMQKIGGGATVSLSTGTLVVMFWAGHGNKNAVETMVKYAAVD
WPKFIDGVHSIGFAPGDQLDGDY..VNAVTREGFKIAHDISYSFVAMAKACRSMI..NPGSALLLTSYLGAERAHPNVNVMGIAKASLPIINVRYMANA

LSPKQIIIVNAVSGGAIDTDALKHFEEREDELEDARQNTIAGRMVEIKDMVDTVEFLV..SSKADMIRGGTIIIVDGGRSLLV-----
LGEFNIRVNAVSGGPIDTDALKAFFDYVEIKEKVEEOSPLKRMGNPNDLAGSAYFLCDETQSGWLICQQTIVVDGGTTFK-----
MGPEGVRVNAISAGPIRILAAASGIKDFRKMLAHCEAVDFIRRTVTIEDVGNSAAFICSDLASAG..ISGEVVHVIGGFSIAAMNELELK

Figure 3